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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/394,020DATE: 01/10/2000
TIME: 23:57:41

INPUT SET: S34406.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

SEQUENCE LISTING

(1) General Information:

Does Not Comply
Corrected Diskette Needed(i) APPLICANT: Pepicelli, Carmen V
Lewis, Paula M
McMahon, Andrew P(ii) TITLE OF INVENTION: Regulation of Lung Tissue by
Hedgehog-like Polypeptides, and Formulations and Uses
Related Thereto

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley, Hoag & Eliot, llp
(B) STREET: One Post Office Square
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII(text)(vi) CURRENT APPLICATION DATA: *US 09/394,020*(A) APPLICATION NUMBER: ~~US 08/099,952~~ → *do not insert prior application
number in*
(B) FILING DATE: ~~10-SEP-1999~~ *OK*
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/099,952
(B) FILING DATE: 11-SEP-1999 *18*

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: HUV-032.01

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000*Current
Application
Data section*

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ERRORED SEQUENCES FOLLOW:

947 (2) INFORMATION FOR SEQ ID NO:8:
948
949 (i) SEQUENCE CHARACTERISTICS:
--> 950 (A) LENGTH: 1191 base pairs 1190 (p.4)
951 (B) TYPE: nucleic acid
952 (C) STRANDEDNESS: both
953 (D) TOPOLOGY: linear
954
955 (ii) MOLECULE TYPE: cDNA
956
957
958 (ix) FEATURE:
959 (A) NAME/KEY: CDS
960 (B) LOCATION: 1..1191
961
962
963 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
964
965 ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG 48
966 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
967 1 5 10 15
968
969 GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG 96
970 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
971 20 25 30
972
973 CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT 144
974 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
975 35 40 45
976
977 GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG 192
978 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
979 50 55 60
980
981 GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC 240
982 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
983 65 70 75 80
984
985 TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC 288
986 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
987 85 90 95
988
989 CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT 336
990 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
991 100 105 110
992

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993	GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC	384
994	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
995	115 120 125	
996		
997	TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC	432
998	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
999	130 135 140	
1000		
1001	CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG TAT GGC	480
1002	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
1003	145 150 155 160	
1004		
1005	TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC	528
1006	Leu Leu Ala Arg Leu Ala Val Glu Ala Phe Asp Trp Val Tyr Tyr	
1007	165 170 175	
1008		
1009	GAG TCC CGC AAC CAC GTC CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG	576
1010	Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
1011	180 185 190	
1012		
1013	GCG GTC CGG GCG GGC GGC TGC TTT CCG GGA AAT GCA ACT GTG CGC CTG	624
1014	Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	
1015	195 200 205	
1016		
1017	TGG AGC GGC GAG CGG AAA GGG CTG CGG GAA CTG CAC CGC GGA GAC TGG	672
1018	Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	
1019	210 215 220	
1020		
1021	GTT TTG GCG GCC GAT GCG TCA GGC CGG GTG GTG CCC ACG CCG GTG CTG	720
1022	Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	
1023	225 230 235 240	
1024		
1025	CTC TTC CTG GAC CGG GAC TTG CAG CGC CGG GCT TCA TTT GTG GCT GTG	768
1026	Leu Phe Leu Asp Arg Asp Leu Gln Arg Ala Ser Phe Val Ala Val	
1027	245 250 255	
1028		
1029	GAG ACC GAG TGG CCT CCA CGC AAA CTG TTG CTC ACG CCC TGG CAC CTG	816
1030	Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	
1031	260 265 270	
1032		
1033	GTG TTT GCC GCT CGA GGG CCG GCG CCC GCG CCA GGC GAC TTT GCA CCG	864
1034	Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	
1035	275 280 285	
1036		
1037	GTG TTC GCG CGC CGG CTA CGC GCT GGG GAC TCG GTG CTG GCG CCC GGC	912
1038	Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	
1039	290 295 300	
1040		
1041	GGG GAT GCG CTT CGG CCA GCG CGC GTG GCC CGT GTG GCG CGG GAG GAA	960
1042	Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	
1043	305 310 315 320	
1044		
1045	GCC GTG GGC GTG TTC GCG CCG CTC ACC GCG CAC GGG ACG CTG CTG GTG	1008

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1046	Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	
1047	325 330 335	
1048		
1049	AAC GAT GTC CTG GCC TCT TGC TAC GCG GTT CTG GAG AGT CAC CAG TGG	1056
1050	Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	
1051	340 345 350	
1052		
1053	GCG CAC CGC GCT TTT GCC CCC TTG AGA CTG CTG CAC GCG CTA GGG GCG	1104
1054	Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala	
1055	355 360 365	
1056		
1057	CTG CTC CCC GGC GGG GCC GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT	1152
1058	Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser	
1059	370 375 380	
1060		
--> 1061	CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC TG	1191
1062	Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly	
1063	385 390 395	
1064		
1065		
1066		

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SEQUENCE VERIFICATION REPORT
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DATE: 01/10/2000
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Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: US 09/099,952
950	Entered (1191) and Calc. Seq. Length (1190) differ	(A) LENGTH: 1191 base pairs
1061	# of Sequences for line conflicts w/ running total	CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CT